
Histone modifications at human enhancers reflect global cell-type-specific gene expression.

Journal: Nature

Publication Year: 2009

Authors: Nathaniel D Heintzman, Gary C Hon, R David Hawkins, Pouya Kheradpour, Alexander Stark, Lindsey F Harp, Zhen Ye, Leonard K Lee, Rhona K Stuart, Christina W Ching, Keith A Ching, Jessica E Antosiewicz-Bourget, Hui Liu, Xinmin Zhang, Roland D Green, Victor V Lobanenko, Ron Stewart, James A Thomson, Gregory E Crawford, Manolis Kellis, Bing Ren

PubMed link: 19295514

Funding Grants: Mapping the transcriptional regulatory elements in the genome of hESC

Public Summary:

The human body is composed of diverse cell types with distinct functions. Although it is known that lineage specification depends on cell-specific gene expression, which in turn is driven by promoters, enhancers, insulators and other cis-regulatory DNA sequences for each gene, the relative roles of these regulatory elements in this process are not clear. We have previously developed a chromatin-immunoprecipitation-based microarray method (ChIP-chip) to locate promoters, enhancers and insulators in the human genome. Here we use the same approach to identify these elements in multiple cell types and investigate their roles in cell-type-specific gene expression. We observed that the chromatin state at promoters and CTCF-binding at insulators is largely invariant across diverse cell types. In contrast, enhancers are marked with highly cell-type-specific histone modification patterns, strongly correlate to cell-type-specific gene expression programs on a global scale, and are functionally active in a cell-type-specific manner. Our results define over 55,000 potential transcriptional enhancers in the human genome, significantly expanding the current catalogue of human enhancers and highlighting the role of these elements in cell-type-specific gene expression.

Scientific Abstract:

The human body is composed of diverse cell types with distinct functions. Although it is known that lineage specification depends on cell-specific gene expression, which in turn is driven by promoters, enhancers, insulators and other cis-regulatory DNA sequences for each gene, the relative roles of these regulatory elements in this process are not clear. We have previously developed a chromatin-immunoprecipitation-based microarray method (ChIP-chip) to locate promoters, enhancers and insulators in the human genome. Here we use the same approach to identify these elements in multiple cell types and investigate their roles in cell-type-specific gene expression. We observed that the chromatin state at promoters and CTCF-binding at insulators is largely invariant across diverse cell types. In contrast, enhancers are marked with highly cell-type-specific histone modification patterns, strongly correlate to cell-type-specific gene expression programs on a global scale, and are functionally active in a cell-type-specific manner. Our results define over 55,000 potential transcriptional enhancers in the human genome, significantly expanding the current catalogue of human enhancers and highlighting the role of these elements in cell-type-specific gene expression.

Source URL: <https://www.cirm.ca.gov/about-cirm/publications/histone-modifications-human-enhancers-reflect-global-cell-type-specific-gene>